

We claim:

1. A method of detecting the expression of a gene in a blood sample, said method comprising the step of detecting in RNA, cDNA or EST from a blood sample, the presence of an RNA, cDNA, or EST complementary to a gene expressed in heart tissue, wherein the detection of said RNA, cDNA or EST is indicative of the expression of said gene in said blood sample.
2. A method for detecting, in a blood sample, a difference in expression of a gene which is expressed in heart tissue, comprising the steps of:
  - a) detecting in a blood sample the presence of RNA, cDNA or EST complementary to a gene expressed in heart tissue;
  - b) comparing the amount of said RNA, cDNA or EST in said sample with the amount of said RNA, cDNA or EST in a blood sample control, wherein detection of a difference in the amount of said RNA, cDNA or EST in said sample compared with said blood sample control indicates a difference in the expression of said gene encoding said RNA, cDNA or EST in said sample.
3. A method for detecting, in a blood sample, expression of a gene expressed in heart tissue, comprising the steps of:
  - a) producing an amplification product from RNA of a blood sample using primers complementary to a gene expressed in heart tissue; and
  - b) detecting the amplification product, wherein detection indicates that the gene is expressed in blood.
4. A method of detecting the expression of a gene in a test subject, comprising the steps of:
  - a) applying primers specific for a gene to a blood sample from a test subject, wherein said gene is expressed in heart tissue; and
  - b) comparing the quantitative expression levels of the gene in said blood sample to expression levels in blood of a control subject, wherein a difference in the expression level of the

gene in said test subject blood sample relative to said control subject blood is indicative of expression of said gene in said test subject.

5. The method of any one of claims 1-4, wherein said gene is a heart tissue-specific gene.
6. The method of any one of claims 1-4, wherein said RNA is quantified.
- 5 7. The method of any one of claims 1-4, wherein said ESTs are generated from RNA from said blood sample.
8. The method of any one of claims 1-4, wherein said ESTs are generated using random sequence primers and gene-specific primers.
9. The method of any one of claims 1-4, wherein said blood sample is a drop of blood.
- 10 10. The method of any one of claims 1-4, wherein said blood sample is from a human.